IN THE SPECIFICATION:

[0019] The amino acid sequence for SC6, can be found in the GenBank database, held by the National Institute of Health (NIH) ~~available at http://www.ncbi.nlm.nih.gov/),~~ under accession number NP.sub.--003034 (SEQ ID No. 1) and the nucleic acid sequence is shown under accession number NM.sub.--003043 (SEQ ID ~~No.~~NO: 2).

[0022] a) comprises or consists of the amino acid sequence of SEQ ID ~~No.~~NO: 1;

[0023] b) is a variant having one or more amino acid substitutions, deletions, insertions or modifications relative to the amino acid sequence of SEQ ID ~~No.~~NO: 1, provided that such variant exhibits the immunological and/or transporter activity of the polypeptide with the amino acid sequence of SEQ ID ~~No.~~NO: 1; or

[0031] a) comprises or consists of the DNA sequence of SEQ ID ~~No.~~NO: 2, or its RNA equivalent;

[0035] e) is a sequence which codes for a variant or fragment of the polypeptide with the amino acid sequence of SEQ ID ~~No.~~NO: 1.

[0111] A polypeptide within the scope of a), may consist of the particular amino acid sequence of SEQ ID ~~No.~~NO: 1 or may have an additional N-terminal and/or an additional C-terminal amino acid sequence relative to the sequence of SEQ ID ~~No.~~NO: 1.

[0115] Whatever additional N-terminal or C-terminal sequence is present, it is preferred that the resultant polypeptide should exhibit the immunological and/or transporter activity of the polypeptide having the amino acid sequence of SEQ ID ~~No.~~NO: 1.

[0117] Turning now to the polypeptides defined in b) above, it will be appreciated by the person skilled in the art that these polypeptides are variants of the polypeptide given in a) above, provided that such variants exhibit the immunological and/or transporter activity of the polypeptide having the amino acid sequence of SEQ ID ~~No.~~NO: 1.

[0133] Whatever amino acid changes are made (whether by means of substitution, insertion, deletion or modification), preferred SC6 polypeptides have at least 50% sequence identity with the polypeptide of SEQ ID ~~No.~~NO: 1, more preferably the degree of sequence identity is at least 75%. Yet more preferably the degree of sequence identity is at least 80% or at least 85%. Sequence identities of at least 90%, or at least 95%, or at least 98% are most preferred.

[0135] The determination of percent identity between two sequences can be accomplished using a mathematical algorithm known to those of skill in the art. An example of a mathematical algorithm for comparing two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. The NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410 have incorporated such an algorithm. BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilised as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilising BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g. XBLAST and NBLAST) can be used. ~~See http://www.ncbi.nlm.nih.gov.~~

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[0212] FIG. 4: shows the expression of SC6 mRNA in seven matched breast tumour tissues. Tumour tissues are designated by (T) and matched normal tissues are designated by (N). SC6 mRNA expression is also shown in breast carcinoma MDA468, BT20, BT474, MCF7 and T47D cells. mRNA levels are expressed as the number of copies ng^{-1} cDNA.

[0228] RT-PCR was used to quantitatively measure SC6 expression in normal human tissue mRNAs (Clontech), and in matched cancer tissues and normal tissue (Clontech). The primers used for PCR were as follows:
2 sense 5' atcggctatgcctccgttgtaa 3' (SEQ ID No.3) antisense 5' agttggtggagctgatggtgat 3' (SEQ ID ~~No.~~NO: 4)